

AMENDMENTS

In the claims:

Please cancel claims 2-5, 33-57, 66-69, 91-94, and 105-134.

Please amend the claims as follows.

1. (Original) A method of determining a comparative expression profile in an individual, comprising:

(a) determining a multidimensional coordinate point representative of the expression levels of a sample of molecules in a population of molecules in a specimen from said individual;

(b) comparing said multidimensional coordinate point to a health-associated reference expression region of said sample of molecules; and

(c) determining if said multidimensional coordinate point is within or outside said health-associated reference expression region, wherein said multidimensional coordinate point within said health-associated reference expression region indicates a reference expression profile and wherein said multidimensional coordinate point outside said health-associated reference expression region indicates a perturbed expression profile.

Claims 2-5 (Canceled).

6. (Original) The method of claim 1, wherein said reference expression profile indicates a reference health state in said individual.

7. (Original) The method of claim 1, wherein said perturbed expression profile indicates a disease state in said individual.

8. (Original) The method of claim 1, wherein said perturbed expression profile indicates the course of a disease.

9. (Original) The method of claim 1, wherein said specimen is selected from the group consisting of leukocytes, blood, and serum.

10. (Original) The method of claim 5, wherein said target is an array.

11. (Original) The method of claim 1, wherein said molecules in said specimen comprise nucleic acids.

12. (Original) The method of claim 5, wherein said target comprises nucleic acid ligands.

13. (Original) The method of claim 1, wherein said molecules in said specimen comprise polypeptides.

14. (Original) The method of claim 5, wherein said target comprises antibody ligands.

15. (Original) The method of claim 1, wherein said molecules in said specimen comprise small molecules.

16. (Original) The method of claim 1, further comprising the step of reporting whether a reference expression profile or a perturbed expression profile is indicated.

17. (Original) A method of determining a comparative expression profile in an individual, comprising comparing the expression levels of a sample of molecules in a population of molecules in a specimen from said individual with health-associated reference expression intervals of said sample of molecules, wherein expression levels within said health-associated reference expression intervals indicate a reference expression profile and wherein expression levels outside said health-associated reference expression intervals indicate a perturbed expression profile.

18. (Original) The method of claim 17, further comprising the step of inputting the expression level of said molecules in said sample.

19. (Original) The method of claim 17, further comprising the step of determining the expression level of said molecules in said sample.

20. (Original) The method of claim 19, wherein the expression levels of said sample of molecules in said specimen are determined by direct comparison with reference expression levels correlated with health-associated reference expression intervals of said molecules in said sample.

21. (Original) The method of claim 19, further comprising the step of contacting said specimen with a target.

22. (Original) The method of claim 17, wherein said reference expression profile indicates a reference health state in said individual.

23. (Original) The method of claim 17, wherein said perturbed expression profile indicates a disease state in said individual.

24. (Original) The method of claim 17, wherein said perturbed expression profile indicates the course of a disease.

25. (Original) The method of claim 17, wherein said specimen is selected from the group consisting of leukocytes, blood, and serum.

26. (Original) The method of claim 17, wherein said target is an array.

27. (Original) The method of claim 17, wherein said molecules in said specimen comprise nucleic acids.

28. (Original) The method of claim 21, wherein said target comprises nucleic acid ligands.

29. (Original) The method of claim 17, wherein said molecules in said specimen comprise polypeptides.

30. (Original) The method of claim 21, wherein said target comprises antibody ligands.

31. (Original) The method of claim 17, wherein said molecules in said specimen comprise small molecules.

32. (Original) The method of claim 17, further comprising the step of reporting whether a reference expression profile or a perturbed expression profile is indicated.

Claims 33-57 (Canceled).

58. (Original) A method of determining a comparative expression profile in an individual, comprising comparing the expression levels of a sample of molecules in a population of molecules in a specimen from said individual with reference expression levels correlated with health-associated reference expression intervals of said sample of molecules, wherein expression levels within said health-associated reference expression intervals indicate a reference expression profile and wherein expression levels outside said health-associated reference expression intervals indicate a perturbed expression profile.

59. (Original) The method of claim 58, further comprising the step of inputting the expression level of said molecules in said sample.

60. (Original) The method of claim 58, further comprising the step of determining the expression level of said molecules in said sample.

61. (Original) The method of claim 58, wherein said reference expression profile indicates a reference health state in said individual.

62. (Original) The method of claim 58, wherein said perturbed expression profile indicates a disease state in said individual.

63. (Original) The method of claim 58, wherein said perturbed expression profile indicates the course of a disease.

64. (Original) The method of claim 58, wherein said specimen is selected from the group consisting of leukocytes, blood and serum.

65. (Amended) A method of diagnosing a [disease] health state, comprising:

(a) determining the expression levels of a sample of molecules in a population of molecules in a specimen from an individual;

(b) comparing said expression levels with a health-associated reference expression region of said sample of molecules; and

(c) determining if said expression levels of said sample of molecules is within or outside said health-associated reference expression region, wherein expression levels within said health-associated reference expression region indicates a reference health state and wherein expression levels outside said health-associated reference expression region indicates a disease state.

Claims 66-69 (Canceled).

70. (Original) The method of claim 65, wherein said reference expression profile indicates a reference health state in said individual.

71. (Original) The method of claim 65, wherein said perturbed expression profile indicates a disease state in said individual.

72. (Original) The method of claim 65, wherein said perturbed expression profile indicates the course of a disease.

73. (Original) The method of claim 65, wherein said specimen is selected from the group consisting of leukocytes, blood, and serum.

74. (Original) The method of claim 69, wherein said target is an array.

75. (Original) The method of claim 65, wherein said molecules in said specimen comprise nucleic acids.

76. (Original) The method of claim 69, wherein said target comprises nucleic acid ligands.

77. (Original) The method of claim 65, wherein said molecules in said specimen comprise polypeptides.

78. (Original) The method of claim 69, wherein said target comprises antibody ligands.

79. (Original) The method of claim 65, wherein said molecules in said specimen comprise small molecules.

80. (Original) The method of claim 65, further comprising the step of reporting whether a reference expression profile or a perturbed expression profile is indicated.

81. (Amended) A method of diagnosing a [disease] health state, comprising:

(a) contacting a specimen with a target;

(b) determining the expression levels of a sample of molecules in a population of molecules in said specimen; and

(c) comparing said expression levels with a health-associated reference expression interval of said sample of molecules, wherein expression levels within said health-associated reference expression interval indicates a reference health state and wherein an expression level outside said health-associated reference expression interval indicates a disease state.

82. (Original) The method of claim 81, wherein said disease state is selected from the group consisting of diabetes and cancer.

83. (Original) The method of claim 81, wherein said specimen is selected from the group consisting of leukocytes, blood, and serum.

84. (Original) The method of claim 81, wherein said target is an array.

85. (Original) The method of claim 81, wherein said molecule in said specimen comprises nucleic acids.

86. (Original) The method of claim 81, wherein said target comprises nucleic acid ligands.

87. (Original) The method of claim 81, wherein said molecule in said specimen comprises polypeptides.

88. (Original) The method of claim 81, wherein said target comprises antibody ligands.

89. (Original) The method of claim 81, wherein said molecules in said specimen comprise small molecules.

90. (Original) A method of diagnosing a health state in an individual, comprising:

(a) determining the expression levels of a sample of molecules in a population of molecules in a specimen from an individual;

(b) comparing said expression levels with a health-associated reference expression region of said sample of molecules; and

(c) determining if said expression levels of said sample of molecules is within or outside said health-associated reference expression region, wherein expression levels within said health-associated reference expression region indicates a reference health state and wherein expression levels outside said health-associated reference expression region indicates a perturbed health state.

Claims 91-94 (Canceled).

95. (Original) The method of claim 90, wherein said perturbed health state indicates a disease state in said individual.

96. (Original) The method of claim 90, wherein said perturbed expression profile indicates the course of a disease.

97. (Original) The method of claim 90, wherein said specimen is selected from the group consisting of leukocytes, blood, and serum.

98. (Original) The method of claim 94, wherein said target is an array.

99. (Original) The method of claim 90, wherein said molecules in said specimen comprise nucleic acids.

100. (Original) The method of claim 94, wherein said target comprises nucleic acid ligands.

101. (Original) The method of claim 90, wherein said molecules in said specimen comprise polypeptides.

102. (Original) The method of claim 94, wherein said target comprises antibody ligands.

103. (Original) The method of claim 90, wherein said molecules in said specimen comprise small molecules.

104. (Original) The method of claim 90, further comprising the step of reporting whether a reference expression profile or a perturbed expression profile is indicated.

Claims 105-134 (Canceled).

135. (Original) A computer apparatus, comprising:

a processor;

main memory in communication with said processor; and

a comparative expression profiler in communication with said main memory
configured to carrying out the computer-executed steps of:

(a) comparing the expression level of a molecule with a health-associated
reference expression interval of said molecule; and

(b) assigning a value of 0 if said expression level is within said
health-associated reference expression interval, assigning a positive numerical value if
said expression level is greater than said health-associated reference expression interval,
or assigning a negative numerical value if said expression level is less than said
health-associated reference expression interval, wherein said expression level within said
health-associated reference expression interval indicates a reference expression profile
and wherein said expression level outside said health-associated reference expression
interval indicates a perturbed expression profile.

136. (Original) The computer apparatus of claim 135, wherein steps (a) and (b)
are repeated one or more times.

137. (Original) The computer apparatus of claim 135, wherein said comparative
expression profiler further is configured to carry out the computer-executed step of determining
said expression level of said molecule.

138. (Original) A computer apparatus, comprising:

a processor;

main memory in communication with said processor; and

a comparative expression profiler in communication with said main memory
configured to carrying out the computer-executed steps of:

(a) determining a multidimensional coordinate point representative of the expression levels of a sample of molecules from an individual; and

(b) comparing said multidimensional coordinate point with a health-associated reference expression region, wherein said multidimensional coordinate point within said health-associated reference expression region indicates a reference expression profile and wherein said multidimensional coordinate point outside said health-associated reference expression region indicates a perturbed expression profile.

139. (Original) The computer apparatus of claim 138, wherein said comparative expression profiler further is configured to carry out the computer-executed step of determining said expression level of said molecule.

140. (Original) A computer-readable medium having stored thereon a plurality of sequences of instructions, said plurality of sequences of instructions including sequences of instructions which, when executed by a processor, cause said processor to perform the steps of:

(a) comparing the expression level of a molecule with a health-associated reference expression interval of said molecule; and

(b) assigning a value of 0 if said expression level is within said health-associated reference expression interval, assigning a positive numerical value if said expression level is greater than said health-associated reference expression interval, or assigning a negative numerical value if said expression level is less than said health-associated reference expression interval, wherein said expression level within said health-associated reference expression interval indicates a reference expression profile and wherein said expression level outside said health-associated reference expression interval indicates a perturbed expression profile.

141. (Original) A computer-readable medium having stored thereon a plurality of sequences of instructions, said plurality of sequences of instructions including sequences of instructions which, when executed by a processor, cause said processor to perform the steps of:

(a) determining a multidimensional coordinate point representative of the expression levels of a sample of molecules from an individual; and

(b) comparing said multidimensional coordinate point with a health-associated reference expression region, wherein said multidimensional coordinate point within said health-associated reference expression region indicates a reference expression profile and wherein said multidimensional coordinate point outside said health-associated reference expression region indicates a perturbed expression profile.

142. (Original) A carrier wave carrying instructions for a processor, said instructions which, when executed by said processor, cause said processor to perform the steps of:

(a) comparing the expression level of a molecule with a health-associated reference expression interval of said molecule; and

(b) assigning a value of 0 if said expression level is within said health-associated reference expression interval, assigning a positive numerical value if said expression level is greater than said health-associated reference expression interval, or assigning a negative numerical value if said expression level is less than said health-associated reference expression interval, wherein said expression level within said health-associated reference expression interval indicates a reference expression profile and wherein said expression level outside said health-associated reference expression interval indicates a perturbed expression profile.

143. (Original) A carrier wave carrying instructions for a processor, said instructions which, when executed by said processor, cause said processor to perform the steps of:

(a) determining a multidimensional coordinate point representative of the expression levels of a sample of molecules from an individual; and

(b) comparing said multidimensional coordinate point with a health-associated reference expression region, wherein said multidimensional coordinate point within said health-associated reference expression region indicates a reference expression profile and wherein said multidimensional coordinate point outside said health-associated reference expression region indicates a perturbed expression profile.

Please add the following new claims.

144. (New) A method of diagnosing a health state in an individual, comprising:

(a) contacting a leukocyte specimen from an individual with a target;

(b) determining the expression levels of a sample of molecules in a population of molecules in said leukocyte specimen;

(c) comparing said expression levels with a health-associated reference expression region of said sample of molecules; and

(d) determining if said expression levels of said sample of molecules is within or outside said health-associated reference expression region, wherein expression levels within said health-associated reference expression region indicates a reference health state and wherein expression levels outside said health-associated reference expression region indicates a perturbed health state.

145. (New) The method of claim 144, wherein said perturbed health state indicates a disease state in said individual.

146. (New) The method of claim 144, wherein said perturbed expression profile indicates the course of a disease.

147. (New) The method of claim 144, wherein said target is an array.

148. (New) The method of claim 144, wherein said molecules in said specimen comprise nucleic acids.

149. (New) The method of claim 144, wherein said target comprises nucleic acid ligands.

150. (New) The method of claim 144, wherein said molecules in said specimen comprise polypeptides.

151. (New) The method of claim 144, wherein said target comprises antibody ligands.

152. (New) The method of claim 144, wherein said molecules in said specimen comprise small molecules.

153. (New) The method of claim 144, further comprising the step of reporting whether a reference expression profile or a perturbed expression profile is indicated.